

SEQUENCE LISTING

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<120> Transgenic Plants with a Modified Activity of a Plastidial ADP/ATP Translocator

<130> 0147-0215P

<140>

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<150> 198 21 442.1 Germany

<151> 1998-05-13

<150> PCT/EP99/03292

<151> 1999-05-12

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sense-primer

<400> 1

cgtgagagat agagagctcg aggtctgat tcaaacc

37

<210> 2

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: antisense-primer

<400> 2

gatacaacag gaatcctgga tgaagc

26

<210> 3

<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 3

gaattcctgc agcccggggg atccactagt ctcgagaagt ggctgggggc ctttcc 56

<210> 4

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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tctagaggcc aaggcggccg cttcaacgga ctgcagtgc 39

<210> 5

<211> 589

<212> PRT

<213> Arabidopsis thaliana

<400> 5

Met Glu Ala Val Ile Gln Thr Arg Gly Leu Leu Ser Leu Pro Thr Lys
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Pro Ile Gly Val Arg Ser Gln Leu Gln Pro Ser His Gly Leu Lys Gln
20 25 30

Arg Leu Phe Ala Ala Lys Pro Arg Asn Leu His Gly Cys Leu Tyr Pro
35 40 45

Leu Thr Gly Thr Arg Asn Phe Lys Pro Leu Ser Gln Pro Cys Met Gly
50 55 60

Phe Arg Phe Pro Thr Lys Arg Glu Ala Pro Ser Ser Tyr Ala Arg Arg
65 70 75 80

Arg Arg Gly Cys Trp Arg Arg Ser Cys Leu Arg Arg Ser Asp Ser Ala
85 90 95

Ala Val Val Ala Ser Arg Lys Ile Phe Gly Val Glu Val Ala Thr Leu
100 105 110

Lys Lys Ile Ile Pro Leu Gly Leu Met Phe Phe Cys Ile Leu Phe Asn
115 120 125

Tyr Thr Ile Leu Arg Asp Thr Lys Asp Val Leu Val Val Thr Ala Lys
130 135 140

Gly Ser Ser Ala Glu Ile Ile Pro Phe Leu Lys Thr Trp Val Asn Leu
145 150 155 160

Pro Met Ala Ile Gly Phe Met Leu Leu Tyr Thr Lys Leu Ser Asn Val
165 170 175

Leu Ser Lys Lys Ala Leu Phe Tyr Thr Val Ile Val Pro Phe Ile Ile
 180 185 190
 Tyr Phe Gly Gly Phe Gly Phe Val Met Tyr Pro Leu Ser Asn Tyr Ile
 195 200 205
 His Pro Glu Ala Leu Ala Asp Lys Leu Leu Thr Thr Leu Gly Pro Arg
 210 215 220
 Phe Met Gly Pro Ile Ala Ile Leu Arg Ile Trp Ser Phe Cys Leu Phe
 225 230 235 240
 Tyr Val Met Ala Glu Leu Trp Gly Ser Val Val Val Ser Val Leu Phe
 245 250 255
 Trp Gly Phe Ala Asn Gln Ile Thr Thr Val Asp Glu Ala Lys Lys Phe
 260 265 270
 Tyr Pro Leu Phe Gly Ile Gly Ala Asn Val Ala Leu Ile Phe Ser Gly
 275 280 285
 Arg Thr Val Lys Tyr Phe Ser Asn Leu Arg Lys Asn Leu Gly Pro Gly
 290 295 300
 Val Asp Gly Ser Phe Val Glu Ser His Asp Glu His Cys Gly Gly Asn
 305 310 315 320
 Gly Thr Arg Ile Cys Leu Ser Ile Gly Gly Ser Asn Arg Tyr Val Pro
 325 330 335
 Leu Pro Thr Arg Ser Lys Asn Lys Lys Glu Lys Pro Lys Met Gly Thr
 340 345 350
 Met Glu Ser Leu Lys Phe Leu Val Ser Ser Pro Tyr Ile Arg Asp Leu
 355 360 365
 Ala Thr Leu Val Val Ala Tyr Gly Ile Ser Ile Asn Leu Val Glu Val
 370 375 380
 Thr Trp Lys Ser Lys Leu Lys Ala Gln Phe Pro Ser Pro Asn Glu Tyr
 385 390 395 400
 Ser Ala Phe Met Gly Ala Phe Ser Thr Cys Thr Gly Val Ala Thr Phe
 405 410 415
 Thr Met Met Leu Leu Ser Gln Tyr Val Phe Asn Lys Tyr Gly Trp Gly
 420 425 430
 Val Ala Ala Lys Ile Thr Pro Thr Val Leu Leu Leu Thr Gly Val Ala
 435 440 445
 Phe Phe Ser Leu Ile Leu Phe Gly Gly Pro Phe Ala Pro Leu Val Ala
 450 455 460
 Lys Leu Gly Met Thr Pro Leu Leu Ala Ala Val Tyr Val Gly Ala Leu
 465 470 475 480

145		150		155		160
Gly Phe Met Leu	Leu Tyr Thr Lys Leu Ser Asn Val Leu Ser Lys Lys					
	165			170		175
Ala Leu Phe Tyr Thr Val Ile Val Pro Phe Ile Val Tyr Phe Gly Ala						
	180			185		190
Phe Gly Phe Val Met Tyr Pro Arg Ser Asn Leu Ile Gln Pro Glu Ala						
	195			200		205
Leu Ala Asp Lys Leu Leu Ala Thr Leu Gly Pro Arg Phe Met Gly Pro						
	210			215		220
Leu Ala Ile Met Arg Ile Trp Ser Phe Cys Leu Phe Tyr Val Met Ala						
	225			230		240
Glu Leu Trp Gly Ser Val Val Val Ser Val Leu Phe Trp Gly Phe Ala						
	245			250		255
Asn Gln Ile Thr Thr Val Asp Glu Ala Lys Lys Phe Tyr Pro Leu Phe						
	260			265		270
Gly Leu Gly Ala Asn Val Ala Leu Ile Phe Ser Gly Arg Thr Val Lys						
	275			280		285
Tyr Phe Ser Asn Met Arg Lys Asn Leu Gly Pro Gly Val Asp Gly Trp						
	290			295		300
Ala Val Ser Leu Lys Ala Met Met Ser Ile Val Val Gly Met Gly Leu						
	305			310		315
Ala Ile Cys Phe Leu Tyr Trp Trp Val Asn Arg Tyr Val Pro Leu Pro						
	325			330		335
Thr Arg Ser Lys Lys Lys Lys Val Lys Pro Gln Met Gly Thr Met Glu						
	340			345		350
Ser Leu Lys Phe Leu Val Ser Ser Pro Tyr Ile Arg Asp Leu Ala Thr						
	355			360		365
Leu Val Val Ala Tyr Gly Ile Ser Ile Asn Leu Val Glu Val Thr Trp						
	370			375		380
Lys Ser Lys Leu Lys Ser Gln Phe Pro Ser Pro Asn Glu Tyr Ser Ala						
	385			390		395
Phe Met Gly Asp Phe Ser Thr Cys Thr Gly Ile Ala Thr Phe Thr Met						
	405			410		415
Met Leu Leu Ser Gln Tyr Val Phe Lys Lys Tyr Gly Trp Gly Val Ala						
	420			425		430
Ala Lys Ile Thr Pro Thr Val Leu Leu Leu Thr Gly Val Ala Phe Phe						
	435			440		445
Ser Leu Ile Leu Phe Gly Gly Pro Phe Ala Pro Leu Val Ala Lys Leu						

450 455 460
 Gly Met Thr Pro Leu Leu Ala Ala Val Tyr Val Val Pro Pro Glu Val
 465 470 475 480
 Ser Ser Ala Arg Val Gln Val Gln His Ser Ser Thr Pro Ser Ala Met
 485 490 495
 Gln Glu Cys Leu Tyr Pro Leu Asp Glu Val Ser Lys Val Lys Ala Lys
 500 505 510
 Leu Gln Leu Met Trp Ser Ala Thr Ile Gly Lys Ser Gly Gly Ala Leu
 515 520 525
 Ile Gln Gln Phe Met Ile Leu Thr Phe Gly Ser Leu Ala Asn Ser Thr
 530 535 540
 Pro Tyr Leu Gly Val Ile Leu Leu Gly Ile Val Thr Ala Trp Leu Ala
 545 550 555 560
 Ala Ala Lys Ser Leu Glu Gly Pro Val
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<210> 7
 <211> 498
 <212> PRT
 <213> Rickettsia prowazekii

<400> 7
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 Ile Trp Pro Ile Glu Gln Tyr Glu Asn Lys Lys Phe Leu Pro Leu Ala
 20 25 30
 Phe Met Met Phe Cys Ile Leu Leu Asn Tyr Ser Thr Leu Arg Ser Ile
 35 40 45
 Lys Asp Gly Phe Val Val Thr Asp Ile Gly Thr Glu Ser Ile Ser Phe
 50 55 60
 Leu Lys Thr Tyr Ile Val Leu Pro Ser Ala Val Ile Ala Met Ile Ile
 65 70 75 80
 Tyr Val Lys Leu Cys Asp Ile Leu Lys Gln Glu Asn Val Phe Tyr Val
 85 90 95
 Ile Thr Ser Phe Phe Leu Gly Tyr Phe Ala Leu Phe Ala Phe Val Leu
 100 105 110
 Tyr Pro Tyr Pro Asp Leu Val His Pro Asp His Lys Thr Ile Glu Ser
 115 120 125
 Leu Ser Leu Ala Tyr Pro Asn Phe Lys Trp Phe Ile Lys Ile Val Gly
 130 135 140

Lys Trp Ser Phe Ala Ser Phe Tyr Thr Ile Ala Glu Leu Trp Gly Thr
 145 150 155 160
 Met Met Leu Ser Leu Leu Phe Trp Gln Phe Ala Asn Gln Ile Thr Lys
 165 170 175
 Ile Ala Glu Ala Lys Arg Phe Tyr Ser Met Phe Gly Leu Leu Ala Asn
 180 185 190
 Leu Ala Leu Pro Val Thr Ser Val Val Ile Gly Tyr Phe Leu His Glu
 195 200 205
 Lys Thr Gln Ile Val Ala Glu His Leu Lys Phe Val Pro Leu Phe Val
 210 215 220
 Ile Met Ile Thr Ser Ser Phe Leu Ile Ile Leu Thr Tyr Arg Trp Met
 225 230 235 240
 Asn Lys Asn Val Leu Thr Asp Pro Arg Leu Tyr Asp Pro Ala Leu Val
 245 250 255
 Lys Glu Lys Lys Thr Lys Ala Lys Leu Ser Phe Ile Glu Ser Leu Lys
 260 265 270
 Met Ile Phe Thr Ser Lys Tyr Val Gly Tyr Ile Ala Leu Leu Ile Ile
 275 280 285
 Ala Tyr Gly Val Ser Val Asn Leu Val Glu Gly Val Trp Lys Ser Lys
 290 295 300
 Val Lys Glu Leu Tyr Pro Thr Lys Glu Ala Tyr Thr Ile Tyr Met Gly
 305 310 315 320
 Gln Phe Gln Phe Tyr Gln Gly Trp Val Ala Ile Ala Phe Met Leu Ile
 325 330 335
 Gly Ser Asn Ile Leu Arg Lys Val Ser Trp Leu Thr Ala Ala Met Ile
 340 345 350
 Thr Pro Leu Met Met Phe Ile Thr Gly Ala Ala Phe Phe Ser Phe Ile
 355 360 365
 Phe Phe Asp Ser Val Ile Ala Met Asn Leu Thr Gly Ile Leu Ala Ser
 370 375 380
 Ser Pro Leu Thr Leu Ala Val Met Ile Gly Met Ile Gln Asn Val Leu
 385 390 395 400
 Ser Lys Gly Val Lys Tyr Ser Leu Phe Asp Ala Thr Lys Asn Met Ala
 405 410 415
 Tyr Ile Pro Leu Asp Lys Asp Leu Arg Val Lys Gly Gln Ala Ala Val
 420 425 430
 Glu Val Ile Gly Gly Arg Leu Gly Lys Ser Gly Gly Ala Ile Ile Gln
 435 440 445

Ser Thr Phe Phe Ile Leu Phe Pro Val Phe Gly Phe Ile Glu Ala Thr
450 455 460

Pro Tyr Phe Ala Ser Ile Phe Phe Ile Ile Val Ile Leu Trp Ile Phe
465 470 475 480

Ala Val Lys Gly Leu Asn Lys Glu Tyr Gln Val Leu Val Asn Lys Asn
485 490 495

Glu Lys